

CC PRIMASE ACTIVITY. SUBUNIT B BINDS TO SUBUNIT A (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- PTM: PHOSPHORYLATION IN A CELL CYCLE-DEPENDENT MANNER.
 CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE ALPHA SUBUNIT B FAMILY.

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CC EMBL: 235795; CAA84855.1; -.
 DR PIR: S45769; S45769.
 DR SGD: 5000031; POL12.
 KW DNA replication; Nucleic acid replication.
 FT DOMAIN: 80
 SEQUENCE 705 AA; 78774 MW; F9F06D12F6979637 CRC64;

Query Match 9.5%; Score 9; DB 1; Length 705;
 Best Local Similarity 100.0%; Pred. No. 0/19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 44 ELLQEFDIS 52
 Db 411 ELLQEFDIS 419

RESULT 4

ID NRFE_ECOLI
 ID NRFE_ECOLI STANDARD: PRT: 552 AA.
 AC P32710;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c-type biogenesis protein nrfe.
 GN NRFE OR B4174.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID:562;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94135626; PubMed=8057835;
 RA Hussain H.A., Grove J., Griffiths L., Busby S., Cole J.;
 RT "A seven-gene operon essential for formate-dependent nitrite
 reduction to ammonia by enteric bacteria.";
 RL Mol. Microbiol. 12:153-163(1994).
 [12]
 SEQUENCE FROM N.A.
 RC MEDLINE=94135626; PubMed=8265357;
 RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
 region from 89.2 to 92.8 minutes.";
 RL Nucleic Acids Res. 21:5408-5417(1993).
 CC -!- FUNCTION: MAY BE REQUIRED FOR THE BIOGENESIS OF C-TYPE
 CYTOCHROMES. POSSIBLE SUBUNIT OF A Heme LIASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Potential).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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DR EMBL: X72298; CAA51045.1; -.
 DR EMBL: U00006; AAC43168.1; -.
 DR EMBL: AE000481; AD13457.1; -.
 DR EcoGene: EG11948; nrfe.
 DR InterPro: IPR002541; CytC_asm.
 DR InterPro: IPR003567; CytC_biolg.
 DR InterPro: IPR003568; CytC_ccmF.
 DR Pfam: PF01578; CytC_asm; 1
 DR PRINTS: PRO1410; CCBIOGENESIS.
 DR TIGRFAMS; TIGR0053; nrfe; 1.
 KW Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 26
 FT TRANSMEM 77 97 46 POTENTIAL.
 FT TRANSMEM 104 124 POTENTIAL.
 FT TRANSMEM 158 178 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 222 242 POTENTIAL.
 FT TRANSMEM 256 276 POTENTIAL.
 FT TRANSMEM 294 314 POTENTIAL.
 FT TRANSMEM 333 353 POTENTIAL.
 FT TRANSMEM 376 396 395 POTENTIAL.
 FT TRANSMEM 399 419 419 POTENTIAL.
 FT TRANSMEM 525 545 POTENTIAL.
 FT TRANSMEM 525 545 POTENTIAL.
 FT CONFLICT 32 32 V -> L (IN REF. 2).
 FT CONFLICT 38 38 A -> G (IN REF. 2).
 FT CONFLICT 190 190 S -> C (IN REF. 2).
 FT CONFLICT 218 218 L -> W (IN REF. 2).
 FT CONFLICT 220 226 RLVVLGS - GWFWDQ (IN REF. 2).
 FT CONFLICT 455 455 A -> G (IN REF. 2).
 FT CONFLICT 481 481 A -> R (IN REF. 2).
 SO SEQUENCE 552 AA; 60884 MW; A0F3410AE6416B CRC64;

Query Match 8.4%; Score 8; DB 1; Length 552;
 Best Local Similarity 100.0%; Pred. No. 1/6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LMLAALL 14
 Db 114 LMLAALL 121

RESULT 5

POLR_ASGP
 ID POLR_ASGP STANDARD: PRT: 2105 AA.
 AC P36309;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Genome poly(A)to[RNA] [Contains: RNA replicase (EC 2.7.7.48); Helicase;
 DE Coat protein].
 OS Apple stem grooving virus (strain P-209) (ASGV); stage: Capillovirus.
 OC Viruses; sRNA positive-strand viruses, no DNA
 OX NCBI_TaxID:36402;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93033167; PubMed=1413530;
 RA Yoshikawa N., Sasaki E., Kato M., Takahashi T.;
 RT "The nucleotide sequence of apple stem grooving capillovirus genome.";
 RC Virology 191:98-105(1992).
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate + N diphosphate ->
 CC (RNA) (N).
 CC -!- PTM: THE N-TERMINAL OF THE COAT PROTEIN IS BLOCKED.
 CC -!- MISCELLANEOUS: THE COAT PROTEIN IS LOCATED IN THE CARBOXY-TERMINAL
 CC REGION OF THIS POLYPROTEIN.

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CC -----
DR EMBL: D14995; BAA03639.1; -;
DR PIR: A44059;
DR MEROPS: C35_001; -;
DR InterPro: IPR001788; RNA_dep_RNAPol2.
DR InterPro: IPR000006; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1; 1.
DR RNA-directed RNA polymerase; Transferase; Polyprotein; ATP-binding;
KW Coat protein; Helicase.
FT NP_BIND 781 788 ATP (POTENTIAL).
FT DOMAIN 1364 1453 POLYMERASE ACTIVE SITE.
SO SEQUENCE 2105 AA; 241240 MW; 331291A5FA137131 CRC64;

Query Match 8.4%; Score 8; DB 1; Length 2105;
Best Local Similarity 100.0%; Pred. No. 4 9; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 43 KELLOEFTI 50
Db 1223 KELLOEFTI 1230

RESULT 6
UCN2_HUMAN STANDARD; PRT: 112 AA.
AC O96RP3; O9BUGO;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE (Uroctin⁺-related peptide).
GN OS
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 111
SEQUENCE FROM N.A.
RX MEDLINE:2122098; PubMed=11329063;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Human stresscopin and stresscopin-related peptide are selective ligands for the type 2 corticotropin-releasing hormone receptor.";
RL Nat. Med. 7:605-611(2001).
RN 121
RP SEQUENCE FROM N.A.
RC TISSUE:Skin and uterus;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

--!- FUNCTION: Suppress food intake, delays gastric emptying and decreases heat-induced edema. Might represent an endogenous ligand for maintaining homeostasis after stress.

--!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-beta.

--!- SUBCELLULAR LOCATION: Secreted.

--!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING FACTOR/UROTENSIN I FAMILY OF PEPTIDES.

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--!- EMBL: AE007668; AAK81652.1; -;
DR InterPro: IPR003682; GiDB.
DR InterPro: IPR000051; SAM_bind.
DR Pfam: PF02527; GiDB; 1.
DR TIGRFAMS: TIGR00138; giDB; 1.
KW Transferase; Methyltransferase; Complete Proteome.

Query Match 7.4%; Score 7; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 8 6; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 YKELLOE 48
Db 29 YKELLOE 35

RESULT 8
TYR_HAEYN STANDARD; PRT: 377 AA.
AC P43902;

DT 01-Nov-1995 (Rel. 32, Created)
 DT 01-Nov-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-protein [Includes: Chorismate mutase (EC 5.4.99.5) (CM); Prephenate dehydrogenase (EC 1.3.1.12) (PDH)].
 GN TYRA OR HIL290.
 OS *Bacteroides*; *Proteobacteria*; gamma subdivision; Pasteurellaceae;
 OC *Haemophilus*.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN="Rd / KNAO / ATCC 51907";
 RX MEDLINE=95350630; PubMed=7542000;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shurtliff S., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RT "whole-genome random sequencing and assembly of *Haemophilus influenzae*"
 RL Science 269:496-512(1995).
 CC -- CATALYTIC ACTIVITY: Chorismate = prephenate + CO(2) + NADH.
 CC -- PATHWAY: Tyrosine biosynthesis.
 CC -- SUBCELLULAR LOCATION: Cytoplasmic.
 CC
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 CC
 CC EMBL: U32809; AAC22939.1; -.
 DR TIGR: H11290; -.
 DR InterPro: IPR002701; Chorismate_mut.
 DR InterPro: IPR003099; PDH.
 DR Pfam: PF01817; Chorismate_mut; 1.
 DR Pfam: PF03153; PDH; 1.
 KW Tyrosine biosynthesis; Isomerase; Oxidoreductase; NAD:
 KW Multifunctional enzyme; Complete proteome.
 FT DOMAIN 1 CHORISMATE MUTASE.
 FT DOMAIN ? PREPHENATE DEHYDROGENASE.
 FT SEQUENCE 377 AA: 43022 MW: 319722CFDEDE5791 CRC64;
 Query Match 7.4%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 54 AAEAMG 60
 Db 59 AAEAMG 65
 RESULT 10
 LEUL-BUCRP STANDARD: PRT: 518 AA.
 ID LEUL-BUCRP
 AC P48571;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase),
 GN LEUA.
 OS Buchnera aphidicola (subsp. *Rhopalosiphum padi*).
 OC Plasmid prep.
 OC Bacteria; *Proteobacteria*; gamma subdivision; *Buchnera*.
 OX NCBI_TaxID=98793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9533198; PubMed=7608990;
 RA Bracho A.M., Martinez-Torres D., Moya A., Latorre A.;
 RT "Discovery and molecular characterization of a plasmid localized in *Buchnera* sp. bacterial endosymbiont of the aphid *Rhopalosiphum padi*";
 RT J. Mol. Evol. 41:67-73(1995).
 CC -- FUNCTION: catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-1,2-oxobutanate (2-isopropylmalate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).
 CC

CC -!- CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanoate + CoA = acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O.

CC -!- PATHWAY: Leucine biosynthesis; first step.

CC -!- SUBNRY: Homocetramer (By similarity).

CC -!- SIMILARITY: BELONGS TO THE ALPHA-TPM SYNTHETASE / HOMOCITRATE SYNTHASE FAMILY. LEUA I SUBFAMILY.

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CC EMBL: X71612; CA50615.1; -

CC Interpro: IPR002034; AIPM/Hicit.synth.

CC Interpro: IPR000891; HMGL-like.

CC ProDom: PRO0682; HMGL-like.

CC TIGRFAMS: TIGR0093; IeuA-Duct; 1.

DR PROSITE: PS00815; AIPM_HOMOCIT_SYNTH_1; 1.

DR PROSITE: PS00816; AIPM_HOMOCIT_SYNTH_2; 1.

KW Leucine biosynthesis; Lyase; Plasmid.

SEQUENCE 518 AA: 57336 MN: 8989C91D5720BA40 CRC64:

Query Match	Best Local Similarity	Score	DB	Length
Oy 53	DAAEAM 59	7.4%	1	518
Db 82	DAAEAM 88	100.0%	0	Mismatches
			0	Indels
			0	Gaps
			0	;

Matches 7; Conservative 100.0%; Pred. No. 16;

RP REVISIONS, AND ALTERNATIVE SPLICING.

RC STRAIN:Berkeley;

RA Mistrak S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celinkier S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Kronmiller B., Marshall B., Milburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whittlefield E.J., Yamada C., Ashburner M., Gelbart W.M., Robin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome.";

RT "Annotation of Drosophila melanogaster genome.";

RL Submitted (May-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.

CC -!- SIMILARITY: BELONGS TO THE ARS2 FAMILY.

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CC EMBL: AE003794; AACM68343.1; -

DR EMBL: AE003784; AACM68345.1; -

KW FlyBase: FBgn003062; CG7843; Hypothetical protein; Alternative splicing.

FT VARPLIC 47 50 MISSING (IN SHCRT ISOFORM).

SEQUENCE 943 AA: 107221 MW: 0C1AF09E0B8AB0B CRC64;

RP SEQUENCE FROM N.A.

STRAIN=Berkeley;

RX MEDLINE:20196006; PubMed=10731132;

RA Adams M.D., Caliner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andreews P., Pfankoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Borrovo D., Botchan M.R., Bouck J., Brokstone P., Brottier P., Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Dahke C., Davenport L.B., Davies P., De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howard T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RESULT 11

ID ARS2_DROME STANDARD; PRT; 943 AA.

AC 03997;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Arsenite-resistance protein 2 homolog.

GN CG7843.

OS Drosophila melanogaster (Fruit fly).

OC Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera;

OC Muscomorpha: Ephydriidea: Drosophilidae: Drosophila.

OX NCBI_TaxID:7272;

RN [1]

RP

RESULT 12

ID GLNE_MYCTU STANDARD; PRT; 994 AA.

AC 010379;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable glutamate-ammonium ligase adenylyltransferase (EC 2.7.7.42) (Glutamine-synthetase adenyltransferase) (ATASE).

GN GN OR RV222C OR MT2279 OR MTCY190.32C OR MTCY427.02C.

OS Mycobacterium tuberculosis.

OC Bacteria: Actinobacteria: Actinobacteria (class); Actinobacteridae: Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OC NCBI_TaxID:1773;

RN [1]

